Claims

1-17 (Cancelled).

18. (withdrawn)

A method for identifying a most likely biological pathway of a set of interacting molecules, wherein said interacting molecules each have one or more conserved features, the method comprising using a computer to execute instructions in a ~~the~~ computer readable medium to perform the steps of:

~~a.~~ representing the set of interacting molecules as oriented network graph, G = <V, E>, where the vertices, V, correspond to molecules, and the edges or connections E, correspond to interactions between molecules;

~~b.~~ assigning a probability P(network) to each possible oriented network graph found from a fixed number of vertices V; and

~~c.~~ selecting an oriented network graph as the most likely biological pathway based on the probabilities P(network) assigned to all possible oriented network graphs, whereby the selected graph provides a molecular interaction network representation of the biological pathway,

wherein step (b) comprises:

(i) assigning an attraction probability p_{ij} to every pair of molecules i and j that the molecules are connected to each other by an oriented edge, and conversely a probability $(1-p_{ij})$ that the molecules are not connected to each other by an oriented edge;

(ii) computing a probability P(E) that a network has a particular edge set E (ε_{ij});

(iii) sorting all the possible oriented network graphs into a finite number of bins, each corresponding to a particular network topology that corresponds to a

particular distribution of edges coming into and out of each vertex in the particular network, so that each bin represents a collection of oriented network graphs characterized by the same network topology;

(iv) computing a probability P(topology) for each bin; and

(v) computing P(network) as the product of P(E) and P(topology).

19. (withdrawn) The method of claim 18, wherein said attraction probabilities p_{ij} are dependent on the conserved features of each molecule and are determined by quantifying the occurrence frequency of said features immediately upstream or downstream of each other within ~~the~~ known networks.

20. (Cancelled)

21. (withdrawn) The method of claim 18, wherein said attraction probabilities p_{ij} are determined by quantifying the number of times conserved features in every pair of molecules i and j are seen in interaction with each other in known networks.

22. (Cancelled).

23. (Cancelled).

24. (Cancelled)

25. (withdrawn) The method of claim 18, further comprising instructions operable to perform the step of obtaining a posterior probability of each possible oriented network graph, and wherein said selected oriented network graph corresponds to the graph having the highest posterior probability.

26. (withdrawn) The method of claim 25, wherein said posterior probability is determined by using Markov Chain Monte Carlo techniques.

27. (withdrawn) The method of claim 18, wherein said interacting molecules are proteins and said conserved features are protein domains or motifs.

28. (withdrawn) The method of claim 27, wherein said conserved features are nucleic acid motifs.

29. (withdrawn) The method of claim 27, wherein said attraction probabilities p_{ij} are determined by quantifying the occurrence frequency of said conserved features at immediately upstream or downstream of each other within the known networks; and said attraction probability p_{ij} of each pair of reaction molecules is determined by quantifying the number of times conserved features in every pair of molecules i and j are seen in interaction with each other in known networks.

30. (Cancelled)

31. (withdrawn) The method of claim 27, wherein said probability P(topology) of each possible network is a product of incoming edge distribution probability and outgoing edge distribution probability within said each possible network; and further comprising step of obtaining posterior probability of each network, wherein said molecular interaction network having the highest network probability is the network having the highest posterior probability, wherein said highest posterior probability is determined by Markov Chain Monte Carlo techniques.

32. (withdrawn) The method of claim 31, wherein said attraction probabilities of said features are determined by quantifying the number of times conserved features in every pair of molecules i and j are seen in interaction with each other within ~~the~~ known networks.

33. (withdrawn) The method of claim 31, wherein said attraction probabilities of said features are determined by quantifying the number of times conserved features in every pair of molecules i and j are seen in interaction with each other within ~~the~~ known networks.

34. (Cancelled)

35. (Cancelled)

36. (Currently Amended) A method for identifying a molecular interaction network representation for a set of interacting molecules within a known biological system, wherein each of said interacting molecules have one or more conserved features, the method comprising using a computer to execute instructions in a computer readable medium to perform the steps of:

~~a.~~ (a) determining attraction probabilities between pairs of molecules of the set of interacting molecules based on known molecular interaction data wherein said determining attraction probabilities ~~are determined by~~ comprises quantifying the occurrence frequency of said conserved features of said pair of molecules immediately upstream or downstream of each other within ~~the~~ known biological system networks;

~~b.~~ (b) determining an edge probability P(E), which is the probability of a single network with a particular edge set, for each possible molecular interaction network of the set of interacting molecules, based on the determined attraction probabilities of each pair of interacting molecules within said each possible molecular interaction network;

~~c.~~ (c) determining a network topology probability P(topology), which is defined as the probability that the network has a particular distribution of edges going into and out of each vertex of the network, for ~~of~~ said each possible molecular interaction network based on the network topology of said network, said topology probability being a product of an incoming edge distribution probability which is the probability the network has a particular distribution of edges going into each vertex of the network and an outgoing edge distribution probability, which is the probability the network has a particular distribution of edges going out of each vertex of the network, within said each possible molecular interaction ~~network.~~ network;

~~d.~~ (d) determining a network probability of said each possible molecular interaction network as a product of said edge probability P(E) and said topology probability P(topology);

~~e.~~ determining a posterior probability of said each possible molecular interaction network using equation 10; and

~~f.~~ identifying the possible molecular interaction network having the highest posterior probability as said molecular interaction network representation for the set of interacting molecules.

37. (Previously presented) The method of claim 36, wherein said molecule is a protein and said conserved features are protein domain or motif.

38. (Currently Amended) A method for identifying a molecular interaction of a molecule within a biological network of interacting molecules, said interacting molecules each having one or more conserved features, the method comprising using a computer to execute instructions in a computer readable medium to perform the steps of:

~~a.~~ identifying a conserved feature of said molecule;

~~b.~~ determining ~~attraction~~ probabilities of attraction between the conserved features of said molecule and other interacting molecules based on known molecular interaction data of the biological network;

~~c.~~ determining ~~molecular interaction~~ probabilities of molecular interactions of said molecule with each of the other interacting molecules based on the ~~attraction~~ probabilities of attraction; ~~and~~

~~d.~~ identifying the molecular interaction of said molecule with one of the other interacting molecules, corresponding to the highest of the determined ~~molecular interaction~~ probabilities of molecular interactions; and

providing the identification of molecular interaction corresponding to the highest of the determined molecular interaction probabilities to a user or further processor.

39. (Previously presented) The method of claim 38, wherein said attraction probabilities of said features are determined by using equation 6 or 14.

40. (previously presented) The method of claim 38, wherein said attraction probabilities of said features are determined by using equation 14.

41. (Previously presented) The method of claim 38, wherein said molecular probability of the molecular interaction between said two molecules is identified by using equations 5 or 17.

42. (Previously presented) The method of claim 38, wherein said likelihood of molecular interactions between said interacting molecules is determined by using equations 17.

43. (Previously Presented) The method of claim 38, wherein said molecules are protein, and said conserved features are protein domain or motif.

44. (Currently Amended) A screening method ~~for identification of~~ for testing whether a compound is capable of modifying the interaction between at least two molecules in a biology network, the method comprising:

~~a.~~ identifying an interaction between said at least two molecules using the method of claim 38;

~~b.~~ introducing ~~a test~~ said compound in the biology network, ~~the test~~ said compound contacting said at least two molecules; and

~~c.~~ comparing the identified interaction of the molecules in the presence of ~~the test~~ said compound with the identified interaction in the absence of ~~the test~~ said compound;

wherein a difference in the identified interaction of the molecules in the presence of ~~the test~~ said compound as compared to the interaction in the absence of a test compound indicates identification of said compound as a compound capable of modifying the interaction between molecules.

45. (Previously Presented) The screening method of claim 44, wherein said molecules are proteins.